

UCT0046P2 sequence.txt  
SEQUENCE LISTING

<110> University of Connecticut Health Center  
Sarfarazi, Mansoor  
Rezaie, Tayebbeh  
Child, Anne H

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Crick, R.P., and Sarfarazi, M.  
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450

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515 520 525

Asp Gln Gln Ala Tyr Leu Val Gln Arg Gly Ala Glu Asp Arg Asp Trp  
530 535 540

Arg Gln Gln Arg Asn Ile Pro Ile His Ser Cys Pro Lys Cys Gly Glu  
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Val Leu Pro Asp Ile Asp Thr Leu Gln Ile His Val Met Asp Cys Ile  
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Ile

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<400> 7

Met Ser His Gln Pro Leu Ser Cys Leu Thr Glu Lys Glu Asp Ser Pro  
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Ser Glu

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UCT0046P2 sequence.txt

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Val Glu Asn His Gln Leu Lys Glu Ala Met Lys Leu Asn Asn Gln Ala  
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Met Lys Gly Arg Phe Glu Glu Leu Ser Ala Trp Thr Glu Lys Gln Lys  
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Glu Glu Arg Leu Leu Phe Glu Met Gln Ser Lys Glu Val Lys Glu Arg  
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Leu Lys Ala Leu Thr His Glu Asn Glu Arg Leu Lys Glu Glu Leu Gly  
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Lys Phe Lys Glu Lys Ser Glu Lys Pro Leu Glu Asp Leu Thr Gly Gly  
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UCT0046P2 sequence.txt

Tyr Arg Tyr Pro Arg Ala Leu Glu Glu Glu Val Glu Lys Leu Lys Thr  
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 Arg Ala Glu Lys Ala Asp Leu Leu Gly Ile Val Ser Glu Leu Gln Leu  
 165 170 175  
 Lys Leu Asn Ser Gly Gly Ser Ser Glu Asp Ser Phe Val Glu Ile Arg  
 180 185 190  
 Met Thr Glu Gly Glu Thr Glu Gly Ala Met Lys Glu Met Lys Asn Cys  
 195 200 205  
 Pro Thr Pro Thr Arg Thr Asp Pro Ile Ser Leu Ser Asn Cys Thr Glu  
 210 215 220  
 Asp Ala Arg Ser Cys Ala Glu Phe Glu Glu Leu Thr Val Ser Gln Leu  
 225 230 235 240  
 Leu Leu Cys Leu Arg Glu Gly Asn Gln Lys Val Glu Arg Leu Glu Val  
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 Ala Leu Arg Glu Ala Lys Glu Arg Ile Ser Asp Phe Glu Lys Lys Ala  
 260 265 270  
 Asn Gly His Ser Ser Thr Glu Lys Gln Thr Ala Arg Arg Ala Asp Arg  
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 Glu Lys Glu Asp Lys Gly Gln Glu Ser Val Gly Ser Glu Val Glu Thr  
 290 295 300  
 Leu Ser Ile Gln Val Thr Ser Leu Phe Lys Glu Leu Gln Glu Ala His  
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 Thr Lys Leu Ser Glu Ala Glu Leu Met Lys Lys Arg Leu Gln Glu Lys  
 325 330 335  
 Cys Gln Ala Leu Glu Arg Lys Asn Ser Ala Thr Pro Ser Glu Leu Asn  
 340 345 350  
 Glu Lys Gln Glu Leu Val Tyr Ser Asn Lys Lys Leu Glu Leu Gln Val  
 355 360 365  
 Glu Ser Met Arg Ser Glu Ile Lys Met Glu Gln Ala Lys Thr Glu Glu  
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370

375

Glu Lys Ser Arg Leu Ala Thr Leu Gln Ala Thr His Asn Lys Leu Leu  
385 390 395 400

Gln Glu His Asn Lys Ala Leu Lys Thr Ile Glu Glu Leu Thr Lys Gln  
405 410 415

Gln Ala Glu Lys Val Asp Lys Met Leu Leu Gln Glu Leu Ser Glu Lys  
420 425 430

Leu Glu Leu Ala Glu Gln Ala Leu Ala Ser Lys Gln Leu Gln Met Asp  
435 440 445

Glu Met Lys Gln Thr Leu Ala Lys Gln Glu Glu Asp Leu Glu Thr Met  
450 455 460

Ala Val Leu Arg Ala Gln Met Glu Val Tyr Cys Ser Asp Phe His Ala  
465 470 475 480

Glu Arg Ala Ala Arg Glu Lys Ile His Glu Glu Lys Glu Gln Leu Ala  
485 490 495

Leu Gln Leu Ala Ile Leu Leu Lys Glu Asn Asn Asp Ile Glu Glu Gly  
500 505 510

Gly Ser Arg Gln Ser Leu Met Glu Met Gln Cys Arg His Gly Ala Arg  
515 520 525

Thr Ser Asp Ser Asp Gln Gln Thr Tyr Leu Phe Gln Arg Gly Ala Glu  
530 535 540

Asp Arg Ser Trp Gln His Gly Gln Gln Pro Arg Ser Ile Pro Ile His  
545 550 555 560

ser Cys Pro Lys Cys Gly Glu Val Leu Pro Asp Ile Asp Thr Leu Gln  
565 570 575

Ile His Val Met Asp Cys Ile Ile  
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UCT0046P2 sequence.txt

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 <309> 2002-03-30  
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 35 40 45

Thr Glu Asn His Gln Leu Lys Glu Ala Met Lys Leu Asn Asn Gln Ala  
 50 55 60

Met Lys Gly Arg Phe Glu Glu Leu Ser Ala Trp Thr Glu Lys Gln Lys  
 65 70 75 80

Glu Glu Arg Gln Phe Phe Glu Thr Gln Ser Lys Glu Ala Lys Glu Arg  
 85 90 95

Leu Met Ala Leu Ser His Glu Asn Glu Lys Leu Lys Glu Glu Leu Gly  
 100 105 110

Lys Leu Lys Gly Lys Ser Glu Arg Ser Ser Glu Asp Pro Thr Asp Asp  
 115 120 125

Ser Arg Leu Pro Arg Ala Glu Ala Glu Gln Glu Lys Asp Gln Leu Arg  
 130 135 140

Thr Gln Val Thr Arg Leu Gln Ala Glu Lys Ala Asp Leu Leu Gly Ile  
 145 150 155 160

Val Ser Glu Leu Gln Leu Lys Leu Asn Ser Ser Gly Ser Ser Glu Asp  
 165 170 175

UCT0046P2 sequence.txt

Ser Phe Val Glu Ile Arg Met Ala Glu Gly Glu Ala Glu Gly Ser Val  
180 185 190

Lys Glu Ile Lys His Ser Pro Gly Pro Thr Arg Thr Val Ser Ile Gly  
195 200 205

Thr Ser Arg Ser Ala Glu Gly Ala Lys Asn Tyr Leu Glu His Glu Glu  
210 215 220

Leu Thr Val Ser Gln Leu Leu Leu Cys Leu Arg Glu Gly Asn Gln Lys  
225 230 235 240

Val Glu Arg Leu Glu Ile Ala Leu Lys Glu Ala Lys Glu Arg Val Ser  
245 250 255

Asp Phe Glu Lys Lys Ala Ser Asn Arg Ser Glu Ile Glu Thr Gln Thr  
260 265 270

Glu Gly Ser Thr Glu Lys Glu Asn Glu Glu Glu Lys Gly Pro Glu Thr  
275 280 285

Val Gly Ser Glu Val Glu Ala Leu Asn Leu Gln Val Thr Ser Leu Phe  
290 295 300

Lys Glu Leu Gln Glu Ala His Thr Lys Leu Ser Glu Ala Glu Leu Met  
305 310 315 320

Lys Lys Arg Leu Gln Glu Lys Cys Gln Ala Leu Glu Arg Lys Asn Ser  
325 330 335

Ala Thr Pro Ser Glu Leu Asn Glu Lys Gln Glu Leu Val Tyr Thr Asn  
340 345 350

Lys Lys Leu Glu Leu Gln Val Glu Ser Met Leu Ser Glu Ile Lys Met  
355 360 365

Glu Gln Ala Lys Thr Glu Asp Glu Lys Ser Lys Leu Ala Met Leu Gln  
370 375 380

Leu Thr His Asn Lys Leu Leu Gln Glu His Asn His Ala Leu Lys Thr  
385 390 395 400

Ile Glu Glu Leu Thr Arg Lys Glu Ser Glu Lys Val Asp Arg Ala Val  
405 410 415

Leu Lys Glu Leu Ser Glu Lys Leu Glu Leu Ala Glu Lys Ala Leu Ala  
420 425 430

UCT0046P2 sequence.txt

Ser Lys Gln Leu Gln Met Asp Glu Met Lys Gln Thr Ile Ala Lys Gln  
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Glu Glu Asp Leu Glu Thr Met Thr Val Leu Arg Ala Gln Met Glu Val  
450 455 460

Tyr Cys Ser Asp Phe His Ala Glu Arg Ala Ala Arg Glu Lys Ile His  
465 470 475 480

Glu Glu Lys Glu Gln Leu Ala Leu Gln Leu Ala Val Leu Leu Lys Glu  
485 490 495

Asn Asp Ala Phe Glu Asp Gly Gly Arg Gln Ser Leu Met Glu Met Gln  
500 505 510

Ser Arg His Gly Ala Arg Thr Ser Asp Pro Asp Gln Gln Ala Tyr Leu  
515 520 525

Val Gln Arg Gly Thr Glu Asp Arg Asp Trp Gln Gln Gln Arg Asn Ile  
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ctgcagcaga tgaaagagct cctgaccgag aaccaccagc tgaaagaagc catgaagcta 420  
aataaccaag ccatgaaagg gcggtttgag gagctttcgg cctggacaga gaaacagaag 480

UCT0046P2 sequence.txt

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UCT0046P2 sequence.txt

<309> 2002-03-30

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Thr Glu Asn His Gln Leu Lys Glu Ala Met Lys Leu Asn Asn Gln Ala  
50 55 60

Met Lys Gly Arg Phe Glu Glu Leu Ser Ala Trp Thr Glu Lys Gln Lys  
65 70 75 80

Glu Glu Arg Gln Phe Phe Glu Thr Gln Ser Lys Glu Ala Lys Glu Arg  
85 90 95

Leu Met Ala Leu Ser His Glu Asn Glu Lys Leu Lys Glu Glu Leu Gly  
100 105 110

Lys Leu Lys Gly Lys Ser Glu Arg Ser Ser Glu Asp Pro Thr Asp Asp  
115 120 125

Ser Arg Leu Pro Arg Ala Glu Ala Glu Gln Glu Lys Asp Gln Leu Arg  
130 135 140

Thr Gln Val Thr Arg Leu Gln Ala Glu Lys Ala Asp Leu Leu Gly Ile  
145 150 155 160

Val Ser Glu Leu Gln Leu Lys Leu Asn Ser Ser Gly Ser Ser Glu Asp  
165 170 175

Ser Phe Val Glu Ile Arg Met Ala Glu Gly Glu Ala Glu Gly Ser Val  
180 185 190

Lys Glu Ile Lys His Ser Pro Gly Pro Thr Arg Thr Val Ser Ile Gly  
195 200 205

Thr Ser Arg Ser Ala Glu Gly Ala Lys Asn Tyr Leu Glu His Glu Glu  
210 215 220

Leu Thr Val Ser Gln Leu Leu Leu Cys Leu Arg Glu Gly Asn Gln Lys  
225 230 235 240

UCT0046P2 sequence.txt

Val Glu Arg Leu Glu Ile Ala Leu Lys Glu Ala Lys Glu Arg Val Ser  
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 Asp Phe Glu Lys Lys Ala Ser Asn Arg Ser Glu Ile Glu Thr Gln Thr  
 260 265 270  
 Glu Gly Ser Thr Glu Lys Glu Asn Glu Glu Glu Lys Gly Pro Glu Thr  
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 Val Gly Ser Glu Val Glu Ala Leu Asn Leu Gln Val Thr Ser Leu Phe  
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 Lys Glu Leu Gln Glu Ala His Thr Lys Leu Ser Glu Ala Glu Leu Met  
 305 310 315 320  
 Lys Lys Arg Leu Gln Glu Lys Cys Gln Ala Leu Glu Arg Lys Asn Ser  
 325 330 335  
 Ala Thr Pro Ser Glu Leu Asn Glu Lys Gln Glu Leu Val Tyr Thr Asn  
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 Lys Lys Leu Glu Leu Gln Val Glu Ser Met Leu Ser Glu Ile Lys Met  
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 Ile Glu Glu Leu Thr Arg Lys Glu Ser Glu Lys Val Asp Arg Ala Val  
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 Ser Lys Gln Leu Gln Met Asp Glu Met Lys Gln Thr Ile Ala Lys Gln  
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 Tyr Cys Ser Asp Phe His Ala Glu Arg Ala Ala Arg Glu Lys Ile His  
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 Glu Glu Lys Glu Gln Leu Ala Leu Gln Leu Ala Val Leu Leu Lys Glu  
 Page 24



Asn Asp Ala Phe Glu Asp Gly Gly Arg Gln Ser Leu Met Glu Met Gln  
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Ser Arg His Gly Ala Arg Thr Ser Asp Pro Asp Gln Gln Ala Tyr Leu  
515 520 525

Val Gln Arg Gly Thr Glu Asp Arg Asp Trp Gln Gln Gln Arg Asn Ile  
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gaccacaag gacagactcc atcatcatgg gcaaatgtac agaggacgcc aggacttg 720  
tggagtttga ggaactgact gtgagccaac tcctgctttg cctcagggaa ggaaaccaa 780  
aggtggagag actcgagatc gcgctcagag aagccaaaga aagaatttca gattttgaaa 840  
agaaagcaaa cgccatttct gcgattgaaa cccagacaga ggggagcaca caaaaagaag 900

UCT0046P2 sequence.txt

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aggaggacaa agaccagag agtgtgggaa tcgaagtga aactctgaac gttcaagtgg 960
cctctctgtt taaggggctt caagaggcgc acacaaagct cagtgaggcc gagctgatga 1020
agaagagact tcaagaaaag tgtcaggctc tggaaaggaa gaactctgca accccatcgg 1080
agctgaatga aaagcaagag ctctgtttaca gtaactggaa gttagagctg cagggtggaga 1140
gcatgcgctc ggaaatcaag atggagcagg ccaagacaga ggaggagaaa tccagggttag 1200
ccactcttca ggcaacacac gacaagctcc ttcaggaaca caataaagct ctgagaacaa 1260
ttgaagaact aaccaaacia caggcagaaa aagtggacaa ggtgcagctg caggagctca 1320
gcgagaagct ggagctggcg gagcaggctc tggcgtccaa gcagctccag atggatgaga 1380
tgaagcagac catcgccaag caggaggagg acctggagac catggccgct ctcagggctc 1440
agatggaggt gtactgttca gatttccatg ctgagagggc agcaaggag aagatccatg 1500
aggaaaagga gcagctggcc ttgcagctcg ccattttgct gaaagagaac aatgactttg 1560
aagatggagg cagtaggcag tccttgatgg aaatgcagtg ccggcacggg gcgagaacca 1620
gcgactctga ccagcaggct tacctgtttc aaagaggagc caaggacatg agctggcagc 1680
atgggcagca gccccggagt attcccattc actcgtgccc caagtgtggg gaggtcctgc 1740
cggacattga cacgcttcag atacatgtga tggactgtat catctga 1787

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<210> 16  
 <211> 586  
 <212> PRT  
 <213> Rattus norvegicus

<300>  
 <308> NM\_145081  
 <309> 2003-04-06  
 <313> (1)..(586)

<400> 16

Met Ser His Gln Pro Leu Ser Cys Leu Thr Glu Lys Gly Asp Ser Ser  
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Cys Glu Thr Pro Gly Asn Gly Pro Ser Asn Met Val His Pro Asn Leu  
20 25 30

Asp Thr Phe Thr Pro Glu Glu Leu Leu Gln Gln Met Lys Glu Leu Leu  
35 40 45

Val Glu Asn His Gln Leu Lys Glu Ala Met Lys Leu Asn Asn Gln Ala  
50 55 60

Met Lys Gly Arg Phe Glu Glu Leu Ser Ala Trp Thr Glu Arg Gln Lys  
65 70 75 80

UCT0046P2 sequence.txt

Glu Glu Arg Gln Leu Phe Glu Ile Gln Ser Lys Glu Ala Lys Glu Arg  
 85 90 95  
 Leu Lys Ala Leu Ser His Glu Asn Glu Arg Leu Lys Glu Glu Leu Gly  
 100 105 110  
 Lys Leu Lys Glu Lys Ser Glu Arg Pro Phe Glu Asp Ile Thr Gly Arg  
 115 120 125  
 Cys Gly Phe Pro Arg Thr Asp Leu Glu Gln Glu Val Gly Ala Thr Glu  
 130 135 140  
 Glu Ala Gly Gly Ala Gly Ser Gly Ala Ser Glu Asp Pro Gly Glu Ala  
 145 150 155 160  
 Pro Ser Gly Leu Arg Lys Arg Thr Leu Leu Gly His Ser Ser Gln Thr  
 165 170 175  
 Ala Ala Gln Ala Gln Leu Arg Arg Leu Leu Arg Arg Leu Leu Arg Gly  
 180 185 190  
 Asp Arg Met Thr Glu Gly Glu Ala Glu Gly Ala Met Lys Glu Met Arg  
 195 200 205  
 Asn Ser Ala Gly Pro Thr Arg Thr Asp Ser Ile Ile Met Gly Lys Cys  
 210 215 220  
 Thr Glu Asp Ala Arg Thr Cys Val Glu Phe Glu Glu Leu Thr Val Ser  
 225 230 235 240  
 Gln Leu Leu Leu Cys Leu Arg Glu Gly Asn Gln Lys Val Glu Arg Leu  
 245 250 255  
 Glu Ile Ala Leu Arg Glu Ala Lys Glu Arg Ile Ser Asp Phe Glu Lys  
 260 265 270  
 Lys Ala Asn Gly His Ser Ala Ile Glu Thr Gln Thr Glu Gly Ser Thr  
 275 280 285  
 Gln Lys Glu Glu Glu Asp Lys Asp Pro Glu Ser Val Gly Ile Glu Val  
 290 295 300  
 Glu Thr Leu Asn Val Gln Val Ala Ser Leu Phe Lys Gly Leu Gln Glu  
 305 310 315 320  
 Ala His Thr Lys Leu Ser Glu Ala Glu Leu Met Lys Lys Arg Leu Gln  
 325 330 335

UCT0046P2 sequence.txt

Glu Lys Cys Gln Ala Leu Glu Arg Lys Asn Ser Ala Thr Pro Ser Glu  
340 345 350

Leu Asn Glu Lys Gln Glu Leu Val Tyr Ser Asn Trp Lys Leu Glu Leu  
355 360 365

Gln Val Glu Ser Met Arg Ser Glu Ile Lys Met Glu Gln Ala Lys Thr  
370 375 380

Glu Glu Glu Lys Ser Arg Leu Ala Thr Leu Gln Ala Thr His Asp Lys  
385 390 395 400

Leu Leu Gln Glu His Asn Lys Ala Leu Arg Thr Ile Glu Glu Leu Thr  
405 410 415

Lys Gln Gln Ala Glu Lys Val Asp Lys Val Gln Leu Gln Glu Leu Ser  
420 425 430

Glu Lys Leu Glu Leu Ala Glu Gln Ala Leu Ala Ser Lys Gln Leu Gln  
435 440 445

Met Asp Glu Met Lys Gln Thr Ile Ala Lys Gln Glu Glu Asp Leu Glu  
450 455 460

Thr Met Ala Val Leu Arg Ala Gln Met Glu Val Tyr Cys Ser Asp Phe  
465 470 475 480

His Ala Glu Arg Ala Ala Arg Glu Lys Ile His Glu Glu Lys Glu Gln  
485 490 495

Leu Ala Leu Gln Leu Ala Ile Leu Leu Lys Glu Asn Asn Asp Phe Glu  
500 505 510

Asp Gly Gly Ser Arg Gln Ser Leu Met Glu Met Gln Cys Arg His Gly  
515 520 525

Ala Arg Thr Ser Asp Ser Asp Gln Gln Ala Tyr Leu Phe Gln Arg Gly  
530 535 540

Ala Lys Asp Met Ser Trp Gln His Gly Gln Gln Pro Arg Ser Ile Pro  
545 550 555 560

Ile His Ser Cys Pro Lys Cys Gly Glu Val Leu Pro Asp Ile Asp Thr  
565 570 575

Leu Gln Ile His Val Met Asp Cys Ile Ile

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 <212> DNA  
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<300>  
 <308> AF513722  
 <309> 2002-06-02  
 <313> (1)..(1799)

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ctgcagcaga tgagagagct tctaatcgag aaccatcagc tgaaagaagc catgaagcta      180
aataatcaag ctatgaaagg gcgatttgag gagctttcag cctggacaga gaagcagaag      240
gaagaacgcc ttttttttga gaccagagc aaagaagcca aagagcgcct aacggctctg      300
agtcttgaaa atgaaaaact gaagcaagaa cttggaaaac taaaaggga aactgaaagg      360
tcatttgagg acctcactgg ggacccaggg gtccccaagg cggaagcaga acaggaagta      420
gaacagctga agaccaggt ggcacgcctt caagctgaaa aggcggatct gctgggcatc      480
gtgtctgaat tgcagctcaa gctgaactca ggtggcccct ctgaagactc ctttgttgaa      540
atcaggatgg ctgagggaga agcagatgca gcaatgaagg aaatcaagac aagtcctggg      600
cccataagaa ctgattccat tgacacgagc aaatctgcag aaggtaccag gaattatttg      660
gaatttgagg aattaactgt gagccagctc ctgctgtgtc taagggaagg aaaccagaag      720
gtggagagac ttgaaatcgc cctcaaggaa gccaaagaaa gaattttaga ttttgaaaag      780
aaagccaagg atcgttctga gactgagacc cagacagaag agcacaaaga acaagagaaa      840
gaagaggaga aaagcccaga aactgttgga agtgaagtgg aaatgttaaa ctttcagggtg      900
acaaccctgt ttaaggagct tcaggaggct cacacgaaac tcagtgaagc tgagctcatg      960
aagaagagac ttcaagaaaa atgtcaggca cttgaaagga aaaattctgc aaccccatca     1020
gagctgaatg aaaagcaaga gcttctttat aataacaaaa agttggagct ccaagtggaa     1080
agcatgagat cagaaattaa aatggagcaa gccaaaacag aagaggaaaa gtccaaatta     1140
actactctac agttgaccca caacaggctt cttcaagaat acaataatgc actgaaaaca     1200
attgaggaac tgaaaagaag agagtctgaa aaagtggata aggtggtgct gcaggaactg     1260
aatggaaagc tggaaatggc agagaaggcc ctggcttcca agcagctcca aatggatgag     1320
atgaagcaga ccattgccaa gcaagagaag gacctggaag ccatggctgt tctcagggtc     1380
cagatggagg tatactgttc tgactttcat gctgaaagag cagcaagaga gaagattcat     1440
gaagaaaagg agcaactggc attgcagctg gcagttttgc tgaaagacga caatgctttt     1500

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UCT0046P2 sequence.txt

gaagagggag ccagcaggca atccttgatg gaaatgcaga gccgtcatgg ggcaagagca 1560  
 agtgatgctg accagcaggc ttttcttggt caaagaggag ctgaggatag aaactggctg 1620  
 caacagcaac aacagaatat tccaattcat tcttgcccca aatgtggaga agttctgcct 1680  
 gacatagata cactactgat tcacgttacg gactgcatca tttaagtgtg gacattttac 1740  
 ttccccaac tgttggtaaa tgtcagattt ttttcccccc aaaaaaaaaa aaaaaaaaaa 1799

<210> 18  
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 <212> PRT  
 <213> Sus scrofa

<300>  
 <308> AF513722  
 <309> 2002-06-02  
 <313> (1)..(574)

<400> 18

Met Ser His Gln Pro Leu Ser Cys Leu Thr Glu Lys Gly Asp Ser Pro  
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Thr Glu Thr Thr Gly Asn Gly Pro Pro Thr Leu Ala His Pro Asn Leu  
 20 25 30

Asp Thr Phe Thr Pro His Glu Leu Leu Gln Gln Met Arg Glu Leu Leu  
 35 40 45

Ile Glu Asn His Gln Leu Lys Glu Ala Met Lys Leu Asn Asn Gln Ala  
 50 55 60

Met Lys Gly Arg Phe Glu Glu Leu Ser Ala Trp Thr Glu Lys Gln Lys  
 65 70 75 80

Glu Glu Arg Leu Phe Phe Glu Thr Gln Ser Lys Glu Ala Lys Glu Arg  
 85 90 95

Leu Thr Ala Leu Ser Leu Glu Asn Glu Lys Leu Lys Gln Glu Leu Gly  
 100 105 110

Lys Leu Lys Gly Lys Thr Glu Arg Ser Phe Glu Asp Leu Thr Gly Asp  
 115 120 125

Pro Arg Val Pro Lys Ala Glu Ala Glu Gln Glu Val Glu Gln Leu Lys  
 130 135 140

Thr Gln Val Ala Arg Leu Gln Ala Glu Lys Ala Asp Leu Leu Gly Ile  
 145 150 155 160

UCT0046P2 sequence.txt

Val Ser Glu Leu Gln Leu Lys Leu Asn Ser Gly Gly Pro Ser Glu Asp  
 165 170 175  
 Ser Phe Val Glu Ile Arg Met Ala Glu Gly Glu Ala Asp Ala Ala Met  
 180 185 190  
 Lys Glu Ile Lys Thr Ser Pro Gly Pro Ile Arg Thr Asp Ser Ile Asp  
 195 200 205  
 Thr Ser Lys Ser Ala Glu Gly Thr Arg Asn Tyr Leu Glu Phe Glu Glu  
 210 215 220  
 Leu Thr Val Ser Gln Leu Leu Leu Cys Leu Arg Glu Gly Asn Gln Lys  
 225 230 235 240  
 Val Glu Arg Leu Glu Ile Ala Leu Lys Glu Ala Lys Glu Arg Ile Leu  
 245 250 255  
 Asp Phe Glu Lys Lys Ala Lys Asp Arg Ser Glu Thr Glu Thr Gln Thr  
 260 265 270  
 Glu Glu His Lys Glu Gln Glu Lys Glu Glu Glu Lys Ser Pro Glu Thr  
 275 280 285  
 Val Gly Ser Glu Val Glu Met Leu Asn Leu Gln Val Thr Thr Leu Phe  
 290 295 300  
 Lys Glu Leu Gln Glu Ala His Thr Lys Leu Ser Glu Ala Glu Leu Met  
 305 310 315 320  
 Lys Lys Arg Leu Gln Glu Lys Cys Gln Ala Leu Glu Arg Lys Asn Ser  
 325 330 335  
 Ala Thr Pro Ser Glu Leu Asn Glu Lys Gln Glu Leu Leu Tyr Asn Asn  
 340 345 350  
 Lys Lys Leu Glu Leu Gln Val Glu Ser Met Arg Ser Glu Ile Lys Met  
 355 360 365  
 Glu Gln Ala Lys Thr Glu Glu Glu Lys Ser Lys Leu Thr Thr Leu Gln  
 370 375 380  
 Leu Thr His Asn Arg Leu Leu Gln Glu Tyr Asn Asn Ala Leu Lys Thr  
 385 390 395 400  
 Ile Glu Glu Leu Lys Arg Arg Glu Ser Glu Lys Val Asp Lys Val Val  
 405 410 415

UCT0046P2 sequence.txt

Leu Gln Glu Leu Asn Gly Lys Leu Glu Met Ala Glu Lys Ala Leu Ala  
 420 425 430  
 Ser Lys Gln Leu Gln Met Asp Glu Met Lys Gln Thr Ile Ala Lys Gln  
 435 440 445  
 Glu Lys Asp Leu Glu Thr Met Ala Val Leu Arg Ala Gln Met Glu Val  
 450 455 460  
 Tyr Cys Ser Asp Phe His Ala Glu Arg Ala Ala Arg Glu Lys Ile His  
 465 470 475 480  
 Glu Glu Lys Glu Gln Leu Ala Leu Gln Leu Ala Val Leu Leu Lys Asp  
 485 490 495  
 Asp Asn Ala Phe Glu Glu Gly Ala Ser Arg Gln Ser Leu Met Glu Met  
 500 505 510  
 Gln Ser Arg His Gly Ala Arg Ala Ser Asp Ala Asp Gln Gln Ala Phe  
 515 520 525  
 Leu Val Gln Arg Gly Ala Glu Asp Arg Asn Trp Leu Gln Gln Gln Gln  
 530 535 540  
 Gln Asn Ile Pro Ile His Ser Cys Pro Lys Cys Gly Glu Val Leu Pro  
 545 550 555 560  
 Asp Ile Asp Thr Leu Leu Ile His Val Thr Asp Cys Ile Ile  
 565 570